



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 | 492,971
Source: 1600
Date Processed by STIC: 6-9-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/492,971

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
- 5 Variable Length The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 6 PatentIn 2.0
 "bug" Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 7 Skipped Sequences
 (OLD RULES) A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences
- 9 Use of n's or Xaa's
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000
- 10 Invalid <213>
 Response Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <220>
- 12 PatentIn 2.0
 "bug" Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 13 Misuse of n/Xaa Sequence(s) _____ missing the <220> "Feature", and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/492,971

DATE: 06/09/2004

TIME: 16:16:32

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\06092004\I492971.raw

3 <110> APPLICANT: Vogel et al., Tikva
 5 <120> TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND USES AND METHODS OF
 PRODUCING SAME

7 <130> FILE REFERENCE: 25775-CZ-AZ-A

9 <140> CURRENT APPLICATION NUMBER: US 09/492,971

10 <141> CURRENT FILING DATE: 2000-01-27

12 <160> NUMBER OF SEQ ID NOS: 38

14 <170> SOFTWARE: PatentIn version 3.1

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 11

18 <212> TYPE: DNA

19 <213> ORGANISM: Synthetic Probe See item 10

21 <400> SEQUENCE: 1

22 ctgtttaaggc a

25 <210> SEQ ID NO: 2

26 <211> LENGTH: 15

27 <212> TYPE: DNA

28 <213> ORGANISM: Synthetic Probe

30 <400> SEQUENCE: 2

31 gacaaaattcg tcttag

34 <210> SEQ ID NO: 3

35 <211> LENGTH: 41

36 <212> TYPE: DNA

37 <213> ORGANISM: Synthetic Probe

39 <400> SEQUENCE: 3

40 tgagaagtgt tttgatcatg ctgctgggac ttccatgtg g

43 <210> SEQ ID NO: 4

44 <211> LENGTH: 43

45 <212> TYPE: DNA

46 <213> ORGANISM: Synthetic Probe

48 <400> SEQUENCE: 4

49 tccgaccaga taggaagtcc cagcagcatg atcaaaacac ttc

52 <210> SEQ ID NO: 5

53 <211> LENGTH: 45

54 <212> TYPE: DNA

55 <213> ORGANISM: Synthetic Probe

57 <400> SEQUENCE: 5

58 tcggagaaac gtgggagaag ccctaccaag gctggatgtat ggttag

61 <210> SEQ ID NO: 6

62 <211> LENGTH: 45

63 <212> TYPE: DNA

64 <213> ORGANISM: Synthetic Probe

66 <400> SEQUENCE: 6

67 acaatctacc atcatccaggc ctggtaggg cttctcccac gtttc

11

15

41

43

45

45

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Input Set : A:\PTO.FG.txt
 Output Set: N:\CRF4\06092004\I492971.raw

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70 <210> SEQ ID NO: 7
71 <211> LENGTH: 45
72 <212> TYPE: DNA
73 <213> ORGANISM: Synthetic Probe
75 <400> SEQUENCE: 7
76 attgtacttg cctggagaa ggcagcggac gcatacttg cactt 45
79 <210> SEQ ID NO: 8
80 <211> LENGTH: 44
81 <212> TYPE: DNA
82 <213> ORGANISM: Synthetic Probe  Same error
84 <400> SEQUENCE: 8
85 ctagaactgc aagtatgcg tccgctgcct tctcccaggc aagt 44
88 <210> SEQ ID NO: 9
89 <211> LENGTH: 38
90 <212> TYPE: DNA
91 <213> ORGANISM: Synthetic Probe
93 <400> SEQUENCE: 9
94 ctcctgttt ctccgttaat gatcctgtaa tatctcac 38
97 <210> SEQ ID NO: 10
98 <211> LENGTH: 33
99 <212> TYPE: DNA
100 <213> ORGANISM: Synthetic Probe
102 <400> SEQUENCE: 10
103 gaatcaagac ctgtttctg tcttcctcta aga 33
106 <210> SEQ ID NO: 11
107 <211> LENGTH: 40
108 <212> TYPE: DNA
109 <213> ORGANISM: Synthetic Probe
111 <400> SEQUENCE: 11
112 ccaggtccct cggaacatca gaaaactgtt attgttggcc 40
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116 <211> LENGTH: 36
117 <212> TYPE: DNA
118 <213> ORGANISM: Synthetic Probe
120 <400> SEQUENCE: 12
121 aattctgtga cacagtggcc ataggaggc tggggg 36
124 <210> SEQ ID NO: 13
125 <211> LENGTH: 42
126 <212> TYPE: DNA
127 <213> ORGANISM: Synthetic Probe
129 <400> SEQUENCE: 13
130 catgaccct tcattggtt tgcatgattc ctctggca gc 42
133 <210> SEQ ID NO: 14
134 <211> LENGTH: 14
135 <212> TYPE: DNA
136 <213> ORGANISM: Synthetic Probe
138 <400> SEQUENCE: 14
139 ctgtttaata agca 14
142 <210> SEQ ID NO: 15

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RAW SEQUENCE LISTING

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143 <211> LENGTH: 2327
 144 <212> TYPE: PRT
 145 <213> ORGANISM: Synthetic Probe, ~~source error~~
 147 <400> SEQUENCE: 15

149 Ser Lys Arg Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala
 150 1 5 10 15
 153 Val Ser Gln Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln
 154 20 25 30
 157 Ile Asn Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys
 158 35 40 45
 161 Thr Cys Tyr Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu
 162 50 55 60
 165 Ala Glu Glu Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val
 166 65 70 75 80
 169 Gly Asp Thr Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr
 170 85 90 95
 173 Cys Ile Gly Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg
 174 100 105 110
 177 Cys His Glu Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg
 178 115 120 125
 181 Pro His Glu Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn
 182 130 135 140
 185 Gly Lys Gly Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp
 186 145 150 155 160
 189 His Ala Ala Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro
 190 165 170 175
 193 Tyr Gln Gly Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser
 194 180 185 190
 197 Gly Arg Ile Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr
 198 195 200 205
 201 Arg Thr Ser Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg
 202 210 215 220
 205 Gly Asn Leu Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp
 206 225 230 235 240
 209 Lys Cys Glu Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly
 210 245 250 255
 213 Pro Phe Thr Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro
 214 260 265 270
 217 Gln Pro Pro Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr
 218 275 280 285
 221 Ser Val Gly Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu
 222 290 295 300
 225 Cys Thr Cys Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr
 226 305 310 315 320
 229 Gln Thr Tyr Gly Gly Asn Leu Asn Gly Glu Pro Cys Val Leu Pro Phe
 230 325 330 335
 233 Thr Tyr Asn Gly Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln
 234 340 345 350
 237 Asp Gly His Leu Trp Cys Ser Thr Ser Asn Tyr Glu Gln Asp Gln

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238	355	360	365
241	Lys Tyr Ser Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Gln Gly		
242	370	375	380
245	Gly Asn Ser Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn		
246	385	390	395
249	400		
His Asn Tyr Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys			
250	405	410	415
253	Trp Cys Gly Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe		
254	420	425	430
257	Cys Pro Met Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val		
258	435	440	445
261	Met Tyr Arg Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His		
262	450	455	460
265	Met Met Arg Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys		
266	465	470	475
269	480		
Ile Ala Tyr Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr			
270	485	490	495
273	Tyr Asn Val Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met		
274	500	505	510
277	Leu Asn Cys Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp		
278	515	520	525
281	Pro Val Asp Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile		
282	530	535	540
285	Gly Asp Ser Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr		
286	545	550	555
289	560		
Cys Tyr Gly Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr			
290	565	570	575
293	Tyr Pro Ser Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro		
294	580	585	590
297	Ser Gln Pro Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser		
298	595	600	605
301	His Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly		
302	610	615	620
305	Arg Trp Lys Glu Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile		
306	625	630	635
309	640		
Lys Gly Leu Lys Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile			
310	645	650	655
313	Gln Gln Tyr Gly His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr		
314	660	665	670
317	Ser Thr Ser Thr Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr		
318	675	680	685
321	Pro Phe Ser Pro Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr		
322	690	695	700
325	Ala Ser Ser Phe Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser		
326	705	710	715
329	720		
Gly Phe Arg Val Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln			
330	725	730	735
333	Tyr Leu Asp Leu Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu		
334	740	745	750

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337 Leu Pro Gly Arg Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp
 338 755 760 765
 341 Gly Glu Gln Ser Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp
 342 770 775 780
 345 Ala Pro Pro Asp Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val
 346 785 790 795 800
 349 Val Arg Trp Ser Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val
 350 805 810 815
 353 Tyr Ser Pro Ser Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu
 354 820 825 830
 357 Thr Ala Asn Ser Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr
 358 835 840 845
 361 Asn Ile Thr Ile Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val
 362 850 855 860
 365 Val Ile Gln Gln Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro
 366 865 870 875 880
 369 Ser Pro Arg Asp Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr
 370 885 890 895
 373 Ile Met Trp Thr Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp
 374 900 905 910
 377 Val Ile Pro Val Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile
 378 915 920 925
 381 Ser Arg Asn Thr Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr
 382 930 935 940
 385 Tyr Tyr Phe Lys Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro
 386 945 950 955 960
 389 Leu Thr Ala Gln Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu Gln
 390 965 970 975
 393 Phe Val Asn Glu Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro Pro
 394 980 985 990
 397 Arg Ala Gln Ile Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg Arg
 398 995 1000 1005
 401 Gly Gln Pro Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr
 402 1010 1015 1020
 405 Pro Leu Arg Asn Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu
 406 1025 1030 1035
 409 Val Ala Ile Lys Gly Asn Gln Glu Ser Pro Lys Ala Thr Gly Val
 410 1040 1045 1050
 413 Phe Thr Thr Leu Gln Pro Gly Ser Ser Ile Pro Pro Tyr Asn Thr
 414 1055 1060 1065
 417 Glu Val Thr Glu Thr Thr Ile Val Ile Thr Trp Thr Pro Ala Pro
 418 1070 1075 1080
 421 Arg Ile Gly Phe Lys Leu Gly Val Arg Pro Ser Gln Gly Gly Glu
 422 1085 1090 1095
 425 Ala Pro Arg Glu Val Thr Ser Asp Ser Gly Ser Ile Val Val Ser
 426 1100 1105 1110
 429 Gly Leu Thr Pro Gly Val Glu Tyr Val Tyr Thr Ile Gln Val Leu
 430 1115 1120 1125
 433 Arg Asp Gly Gln Glu Arg Asp Ala Pro Ile Val Asn Lys Val Val

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

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Output Set: N:\CRF4\06092004\I492971.raw